receptor tyrosine kinase ECD), MusK (human muscle specific receptor tyrosine kinase ECD), NpoR (human orphan receptor NpoR ECD), Rse (human receptor tyrosine kinase, Rse, ECD), HER3 (human receptor tyrosine kinase HER3/c-erbB3 ECD), Ob-R (human leptin receptor ECD), and VEGF (human vascular endothelial growth factor) where ECD refers to the extracellular domain. The nucleotide sequence data for scFv fragments from populations of antibodies raised to each antigen was translated to derive corresponding protein sequences. The V_L sequences were then compared using the program "align" with the algorithm of Feng and Doolittle (1985, 1987, 1990) to calculate the percentage identity between all pairwise combinations of chains (Feng, D.F. and Doolittle, R.F. (1985) J. Mol. Evol. 21:112-123; Feng, D.F. and Doolittle, R.F. (1987) J. Mol. Evol. 25:351-360; and Feng,D.F. and Doolittle, R.F. (1990) Methods Enzymol. 183:375-387). The percent sequence identity results of each pairwise light chain amino acid sequence comparison were arranged in matrix format (See Table 6.1 - 6.15)

Please cancel Appendix pages 1-15 found after page 103 and insert the appendix now labeled as Tables 6.1-6.15 on page 103 immediately after line 15.

IN THE CLAIMS

Please amend claims 30, 33, 39, 41, and 43 as follows:

30. (AMENDED) A method of preparing a multispecific antibody comprising a first polypeptide and at least one additional polypeptide, wherein

(a) the first polypeptide comprises a multimerization domain forming an interface positioned to interact with an interface of a multimerization domain of the additional polypeptide,

(b) the first and additional polypeptides each comprise a binding domain, the binding domain comprising a heavy chain and a light chain, wherein the variable light chains of the first and additional polypeptides have at least 80% sequence identity, the method comprising the steps of: